M ₁₁₀ (1-38)peptide	26	PPVV <u>krok</u> tkvkf	38 SEQ ID. NO: 3
$G_{\mathtt{L}}$	52	TVQE <u>KK</u> V <u>K</u> K <u>RVSF</u> ADQGL	69 SEQ ID. NO: 4
G _M (63-93)peptide	63	GRRVSFADNFG	73 SEQ ID NO: 5

Fig. 5

G _L 132 R5 157 R6 177 G _M 128 GAC1 244 'AMYL 33 Consensus	VOIDSYNYDGSTESGKIYYKNIAYSKKYTYIYADGSDNWNNG VCLENCSLGESTYTGIYKYNIASEEKVYKIRMTFDTWKSFT VCLENCSLGESTYTGIYKYNIASEEKVYLTITFNSWRDIH VKLHSLTQLGDSSKITGLYYYKNIASEEKVYLTILTFNSWRDIH VKLHSLTQLGDSSKITGLYYYKNIASEEKVYLTILTFNSWRDIH VKLHSLTQLGDSSKITGLYYYKNIASEEKVYLTILTFNSWRDIH VKLHSLTQLGDSSKITGLYYYKNIASEEKVYLTILAH VKLHSLTQLGSDNWNNG	172 SEQ ID. NO: 6 197 SEQ ID. NO: 7 217 SEQ ID. NO: 8 170 SEQ ID. NO: 9 287 SEQ ID. NO: 10 75 SEQ ID. NO: 11
	$\phi.\overline{g}.\overline{V}.\overline{N}\phi.\overline{F}.\overline{K}.\overline{V}.\overline{V}.\overline{\phi}.\dots.\overline{\overline{W}}$	
PHOS 398	RHIQIIYEINQRFINRVAAAFPGDVDRLRRMS	429 SEQ ID. NO: 12
	** ***	
G _L 173 R5 198 R6 218 G _M 171 GAC1 288 AMYL 76 Consensus PHOS 330	DFPCQYVKDTYAGSDRDTFSEDISLPEKIQSYE	205 .230 251 203 331 104
R5 231 R6 252 G _M 204 GAC1 332	L FY L FY	231 256 282 229 360 128

Fig. 6